

FIG. 1

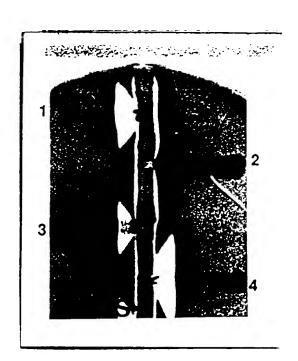


FIG. 3B

FIG. 3A

A?	carartararatarataratatatatatatararcacatatat <u>tigac</u> -35	09
7.7.L	+1 >TTGTTACTG <u>TATGA</u> TACAGGCATAAGTACTTATTTATTATAGATTGCAA -10	120
··	SAATTATATTTTCA <u>AAGAGG</u> AATGCTT ATG GAA TTC AAA AAG TTA CTT TAT SD Met Glu Phe Lys Lys Leu Leu Tyr a SIGNAL PEPTIDE a a	180 8
T. Jeu	3GT TCA ATC GCA GGA ATT ACT TTA TTT TCC CCA ATT TTA ACA AGT GTC CAA GCA Gly Ser Ile Ala Gly Ile Thr Leu Phe Ser Pro Ile Leu Thr Ser Val Gln Ala>a_a_a_a_a_a_a_a_a_a_a_a_a_a_a_a_a_	240 28
LS:	ATA AAT GTT AGT CAA CCA TCT AAT AAT GAA AGT AAT GTT ATT TCA CAG AAA AAA Ile Asn Val Ser Gln Pro Ser Asn Asn Glu Ser Asn Val Ile Ser Gln Lys Lys> bbbb MATURE PEPTIDE_bbbbbbbbb	300 48
	ATT GAT AAT AGT CTA AAT CAG GAA AGT GCT CAA CTA TAT GCC TTG AAA GAA GAT Ile Asp Asn Ser Leu Asn Gln Glu Ser Ala Gln Leu Tyr Ala Leu Lys Glu Asp>	360 68
31 : 7a :	GGA ACT GAG AAA GAA CAA TCA GTT AAT TCA GCA ATT TCA GCT GTT GAA AAT TTA Gly Thr Glu Lys Glu Gln Ser Val Asn Ser Ala Ile Ser Ala Val Glu Asn Leu>	420 88

^ q _ q	ACA AAT 540 Thr Asn> 128	TT CGC ATT 600 le Arg Ile> 148 b>	CAA GTG 660 Gln Val> 168	TAC GTT 720 Tyr Val> 188	GTT CTT 780 Val Leu> 208 >b>	GTA GGT 840 Val Gly> 228 2b>
b b b b b MATURE PEPTIDE b b b b b b b	CAA GCA ATT GTT TTT TCA ACG CAA CAG TTA ACA AAT Gln Ala Ile Val Phe Ser Thr Gln Gln Leu Thr Asn> MATURE PEPTIDE_bb_b_b_b_bb	ASP GAR GCT CAC ATT GAT ATG GGA TTT GCT ATT ACG AAA TTA CTT ATT CGC ATT SEP GIN Ala His Ile ASP Met Gly Phe Ala Ile Thr Lys Leu Leu Ile Arg Ile> B b b b b b MATURE PEPTIDE b b b b b b c c c c c c c c c c c c c	CA TTT GCT TCA AAT GAA TCC ATT AAA GGG CAA GTC GAA GCT GTT AAA CAA GTG Pro Phe Ala Ser Asn Glu Ser Ile Lys Gly Gln Val Glu Ala Val Lys Gln Val>	CTT ACC TAT CCC GAT TTG CAG CCT ACG GAT AGA GCA ACT ATT TAC GTT Leu Thr Tyr Pro Asp Leu Gln Pro Thr Asp Arg Ala Thr Ile Tyr Val> b b b b b b b b b b b b c b c c c c c c	AAA TTA GAC AAG CTT ATT TGG CAA ACA AGA ATT ACC AGA GAT CAA AAA GTT CTT Lys Leu Asp Lys Leu Ile Trp Gln Thr Arg Ile Thr Arg Asp Gln Lys Val Leu> b b b b b b b AATURE PEPTIDE b b b b b b b c b c c c c c c c c c c	AAG AGT TTT GAA GTT TAT CAT CAA TTA AAT AAA GCT ATC ACA CAT GCA GTA GGT Lys Ser Phe Glu Val Tyr His Gln Leu Asn Lys Ala Ile Thr His Ala Val Gly> b b b b b b b mATURE PEPTIDE b b b b b b b b b b b b b b b b b b b
URE PEPTIDE_bb_	GCA ATT GTT TTT TO Ala Ile Val Phe So URE PEPTIDE_bb	ATG GGA TTT GCT ATT ACG AAA TTA CTT AT Met Gly Phe Ala Ile Thr Lys Leu Leu I MATURE PEPTIDE_bb_b_b	ATT AAA GGG CAA G' Ile Lys Gly Gln V URE PEPTIDE_bb	TTG CAG CCT ACG G Leu Gln Pro Thr A URE PEPTIDE_bb_	CAA ACA AGA ATT A Gln Thr Arg Ile T URE PEPTIDE_bb_	CAA TTA AAT AAA G Gln Leu Asn Lys A URE PEPTIDE_bb_
b b mar	CA ATC TCT GAC GTG ATT CAA GCA	r cac arr gar arg a His Ile Asp Met b_b_b MAT	T TCA AAT GAA TCC a Ser Asn Glu Ser bb MAT	T ACC TAT CCC GAT u Thr Tyr Pro Asp b_b_ h_ MAT	C AAG CTT ATT TGG p Lys Leu Ile Trp b b MAT	r GAA GTT TAT CAT e Glu Val Tyr His b_b_b_mAT
	CA ATC TCI la Ile Ser b b	ASP CAA GCT	CA TTT GCT Pro Phe Ale	ACT GTG CTJ Thr Val Let	AAA TTA GA(Lys Leu Asr	AAG AGT TTT Lys Ser Phe
ο 	TE :	AAA.	, , , , , , , , , , , , , , , , , , ,	Ai	AA); 	AA

JTA.	TA AAT CCA ACT GTA ACA GTT GCA CAA GTT GAC CAA GAA ATC AAA GTG CTA CAA eu Asn Pro Thr Val Thr Val Ala Gln Val Asp Gln Glu Ile Lys Val Leu Gln> b b b b b MATURE PEPTIDE b b b b b b c caa	900
347	TA AAT ACT GCT CTA CAG TAAGGTAGAGATTGAATTGA	960
	PTAATTTCAGTCCTTTAGAATTTTTATTTAGCTGATTTACTTGTTGAAGAGA	1020
.T.	AAAATCAAGTACCATACTTCTTCTCCTCCAAATACTTGTATGTCGATTCC	1080
,	ACATAGCTAATTAGTTTTCTGGCTAATAGATTGTACATGAAATTGTT	1140
SAF	CTAGGGTAAAAGGTTTTTTTTTTATAAATTCATGACTAT	1190

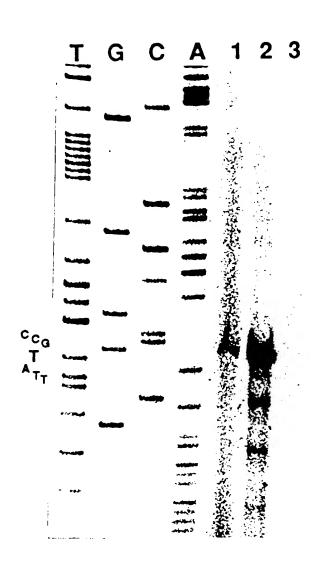


FIG. 5

SUCAMP	1	MEFKKLLYLTGSIAGITLFSPILTSVQANQINVSQP	-45
SAGCAMP	1	DQVTTPQVVNHVNSNNQAQQMA -22	-22
SUCAMP	ı	QKKEEIDNSLNQESAQLYALKEDVKGTEKEQSVNSAISAVENLKTSLRAN -95	-95
SAGCAMP	1	OKLDQDSIQLRNIKDNVQGTDYEKPVNEAITSVEKLKTSLRAN -65	-65
SUCAMP	ł	PETIYDLNSIGTRVEAISDVIQAIVFSTQQLTNKVDQAHIDMGFAITKLL -145	-145
SAGCAMP	ı	SETVYDLNSIGSRVEALTDVIEAITFSTQHLANKVSQANIDMGFGITKLV -115	-115
SUCAMP	ı	IRIADPFASNESIKGQVEAVKQVQATVLTYPDLQPTDRATIYVKSKLDKL -195	-195
SAGCAMP	1	IRILDPFASVDSIKAQVNDVKALEQKVLTYPDLKPTDRATIYTKSKLDKE	-165
SUCAMP	1	IWQTRITRDQKVLNVKSFEVYHQLNKAITHAVGVQLNPTVTVAQVDQEIK -245	-245
SAGCAMP	1	IWNTRFTRDKKVLNVKEFKVYNTLNKAITHAVGVQLNPNVTVQQVDQEIV -215	-215
SUCAMP	I	VLQEALNTALQ -256	
SAGCAMP	1	i.i.i. Tloaalqtalk -226	

12345678



F/G. 7

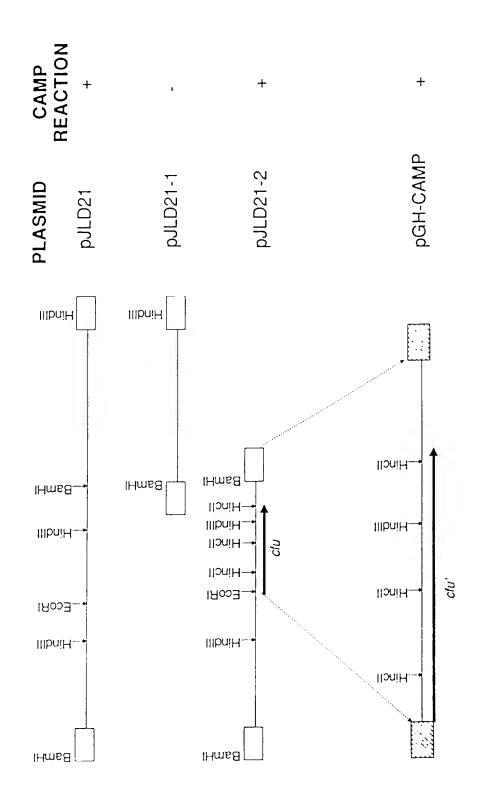


FIG. 8